



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:34 AM UTC

PDB ID : 6KEX / pdb_00006kex
Title : Crystal structure of reduced phosphoribulokinase from Arabidopsis thaliana
Authors : Yu, A.; Xie, Y.; Li, M.
Deposited on : 2019-07-05
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

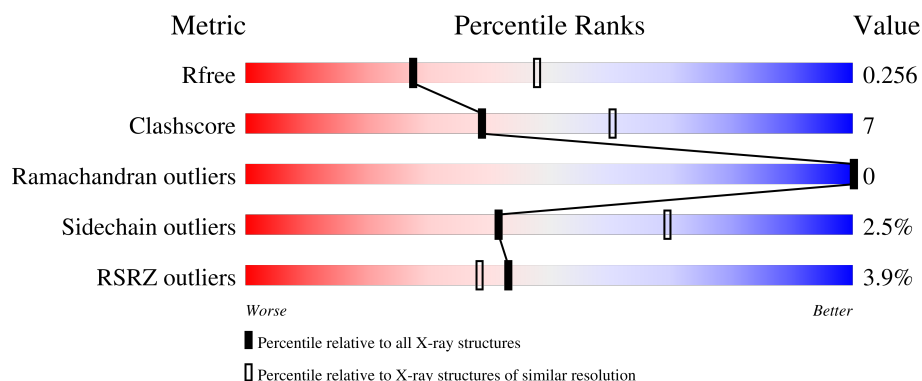
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	359	6% 77% 20% .
1	B	359	4% 79% 16% ..
1	C	359	4% 80% 14% ..
1	D	359	2% 78% 18% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11114 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Phosphoribulokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2756	1756	460	529	11			
1	B	343	Total	C	N	O	S	0	0	0
			2718	1733	453	521	11			
1	C	343	Total	C	N	O	S	0	0	0
			2718	1733	453	521	11			
1	D	347	Total	C	N	O	S	0	0	0
			2746	1750	458	527	11			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP P25697
A	2	GLY	-	expression tag	UNP P25697
A	352	LEU	-	expression tag	UNP P25697
A	353	GLU	-	expression tag	UNP P25697
A	354	HIS	-	expression tag	UNP P25697
A	355	HIS	-	expression tag	UNP P25697
A	356	HIS	-	expression tag	UNP P25697
A	357	HIS	-	expression tag	UNP P25697
A	358	HIS	-	expression tag	UNP P25697
A	359	HIS	-	expression tag	UNP P25697
B	1	MET	-	expression tag	UNP P25697
B	2	GLY	-	expression tag	UNP P25697
B	352	LEU	-	expression tag	UNP P25697
B	353	GLU	-	expression tag	UNP P25697
B	354	HIS	-	expression tag	UNP P25697
B	355	HIS	-	expression tag	UNP P25697
B	356	HIS	-	expression tag	UNP P25697
B	357	HIS	-	expression tag	UNP P25697
B	358	HIS	-	expression tag	UNP P25697
B	359	HIS	-	expression tag	UNP P25697
C	1	MET	-	expression tag	UNP P25697

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Chain	Residue	Modelled	Actual	Comment	Reference
C	2	GLY	-	expression tag	UNP P25697
C	352	LEU	-	expression tag	UNP P25697
C	353	GLU	-	expression tag	UNP P25697
C	354	HIS	-	expression tag	UNP P25697
C	355	HIS	-	expression tag	UNP P25697
C	356	HIS	-	expression tag	UNP P25697
C	357	HIS	-	expression tag	UNP P25697
C	358	HIS	-	expression tag	UNP P25697
C	359	HIS	-	expression tag	UNP P25697
D	1	MET	-	expression tag	UNP P25697
D	2	GLY	-	expression tag	UNP P25697
D	352	LEU	-	expression tag	UNP P25697
D	353	GLU	-	expression tag	UNP P25697
D	354	HIS	-	expression tag	UNP P25697
D	355	HIS	-	expression tag	UNP P25697
D	356	HIS	-	expression tag	UNP P25697
D	357	HIS	-	expression tag	UNP P25697
D	358	HIS	-	expression tag	UNP P25697
D	359	HIS	-	expression tag	UNP P25697

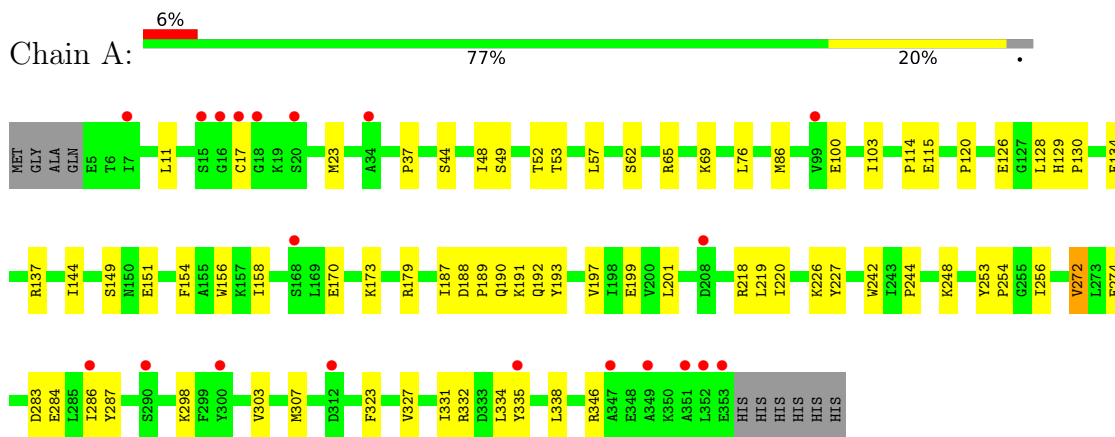
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	50	Total O 50 50	0	0
2	B	44	Total O 44 44	0	0
2	C	38	Total O 38 38	0	0
2	D	44	Total O 44 44	0	0

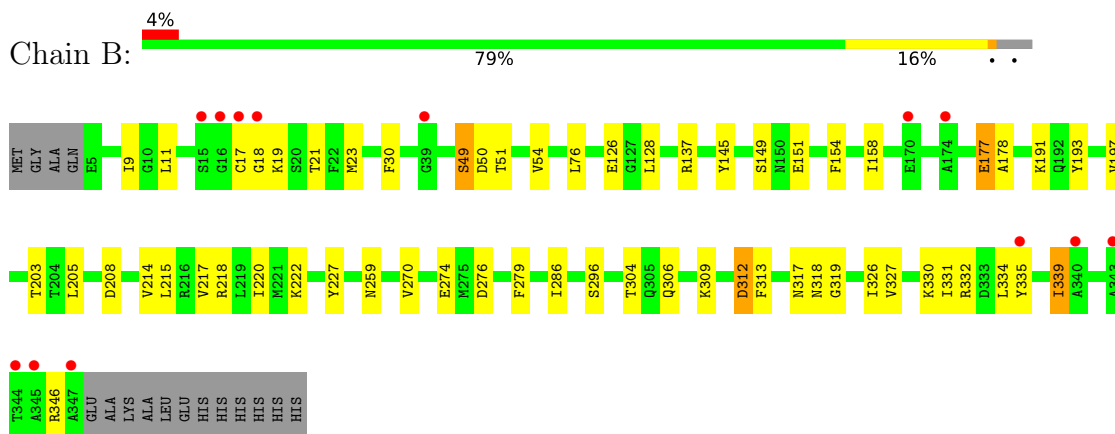
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

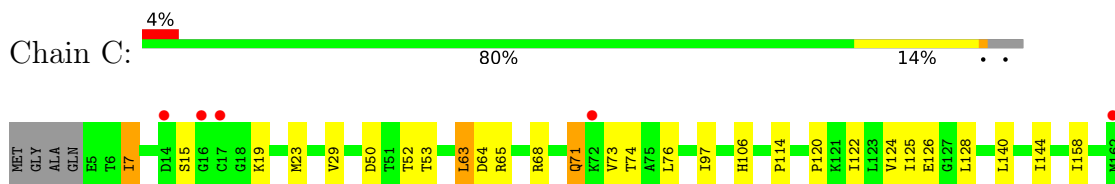
• Molecule 1: Phosphoribulokinase

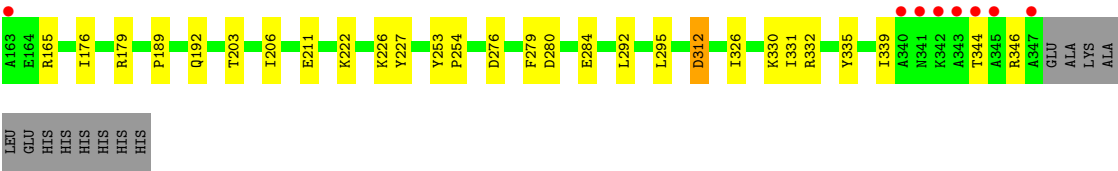


• Molecule 1: Phosphoribulokinase

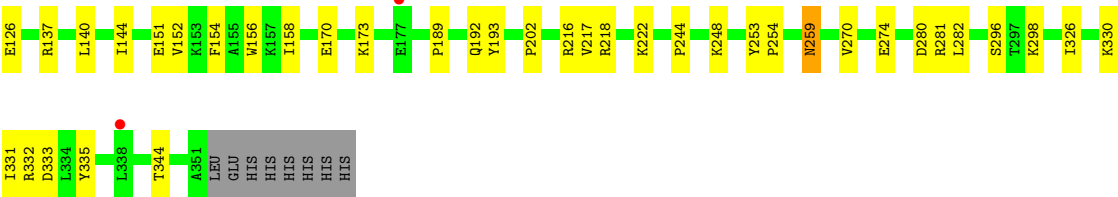
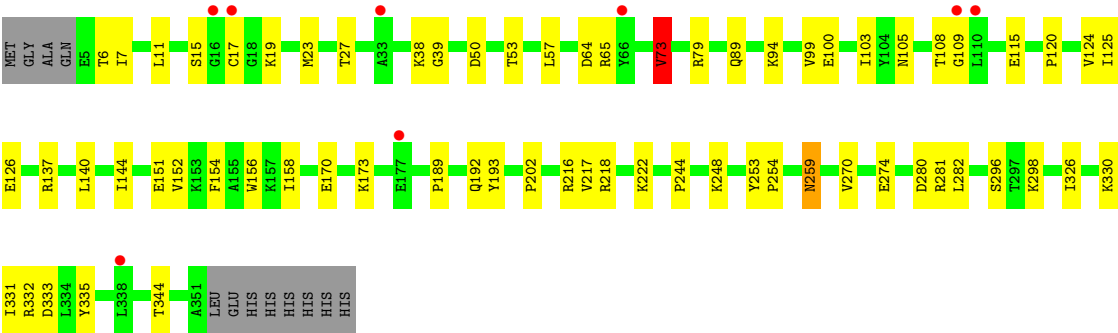
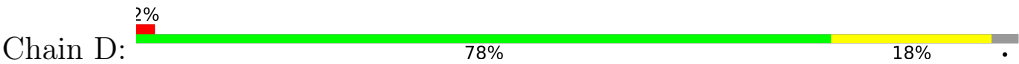


• Molecule 1: Phosphoribulokinase





● Molecule 1: Phosphoribulokinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.84Å 80.36Å 103.09Å 70.10° 82.26° 89.85°	Depositor
Resolution (Å)	49.33 – 2.50 49.33 – 2.50	Depositor EDS
% Data completeness (in resolution range)	94.5 (49.33-2.50) 95.2 (49.33-2.50)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.211 , 0.256 0.211 , 0.256	Depositor DCC
R_{free} test set	5112 reflections (9.43%)	wwPDB-VP
Wilson B-factor (Å ²)	45.0	Xtriage
Anisotropy	0.278	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11114	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 59.79 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6747e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.29	0/2815	0.45	0/3812
1	B	0.20	0/2777	0.41	0/3761
1	C	0.27	0/2777	0.43	0/3761
1	D	0.28	0/2805	0.47	1/3798 (0.0%)
All	All	0.26	0/11174	0.44	1/15132 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	73	VAL	N-CA-C	9.81	124.30	108.99

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2756	0	2727	41	0
1	B	2718	0	2694	37	0
1	C	2718	0	2694	35	0
1	D	2746	0	2723	36	0
2	A	50	0	0	0	0
2	B	44	0	0	0	0
2	C	38	0	0	0	0
2	D	44	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	11114	0	10838	147	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (147) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:THR:HG22	1:C:122:ILE:HB	1.66	0.78
1:B:203:THR:HG22	1:B:205:LEU:H	1.49	0.77
1:C:74:THR:HG23	1:C:76:LEU:H	1.50	0.76
1:C:7:ILE:HG21	1:C:339:ILE:HD11	1.68	0.76
1:C:23:MET:HE1	1:C:124:VAL:HG11	1.69	0.75
1:A:144:ILE:HD11	1:A:331:ILE:HD11	1.67	0.75
1:D:23:MET:HE1	1:D:124:VAL:HG11	1.69	0.74
1:C:71:GLN:HB3	1:C:73:VAL:HG22	1.76	0.68
1:A:114:PRO:HD2	1:C:97:ILE:HD12	1.78	0.66
1:D:89:GLN:NE2	1:D:100:GLU:O	2.31	0.64
1:B:332:ARG:HA	1:B:335:TYR:CE2	2.33	0.64
1:D:216:ARG:NH2	2:D:402:HOH:O	2.31	0.63
1:A:149:SER:HB3	1:A:201:LEU:HD23	1.81	0.62
1:A:332:ARG:HA	1:A:335:TYR:CE2	2.33	0.62
1:C:7:ILE:CG2	1:C:339:ILE:HD11	2.31	0.60
1:C:332:ARG:HA	1:C:335:TYR:CE2	2.37	0.60
1:A:170:GLU:HA	1:A:173:LYS:HE2	1.83	0.60
1:D:222:LYS:HA	1:D:270:VAL:HG12	1.84	0.59
1:A:218:ARG:HG2	1:A:274:GLU:HG2	1.85	0.59
1:A:100:GLU:HG3	1:A:114:PRO:HB2	1.83	0.59
1:D:105:ASN:HB3	1:D:108:THR:HG22	1.84	0.59
1:C:125:ILE:HD11	1:C:140:LEU:HD21	1.85	0.58
1:A:53:THR:HB	1:A:120:PRO:HG3	1.86	0.57
1:D:280:ASP:OD1	1:D:281:ARG:HG3	2.05	0.57
1:B:19:LYS:HD2	1:B:126:GLU:OE2	2.04	0.57
1:B:306:GLN:HA	1:B:309:LYS:HD2	1.86	0.56
1:A:226:LYS:HE3	1:A:227:TYR:CZ	2.40	0.56
1:C:206:ILE:HD11	1:C:254:PRO:HG3	1.87	0.56
1:A:256:ILE:HD11	1:A:284:GLU:HB3	1.88	0.56
1:D:6:THR:OG1	1:D:94:LYS:HA	2.05	0.55
1:D:332:ARG:HA	1:D:335:TYR:CE2	2.41	0.55
1:D:53:THR:HB	1:D:120:PRO:HG3	1.87	0.55
1:C:7:ILE:HG21	1:C:339:ILE:CD1	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:LEU:HD12	1:B:318:ASN:HD21	1.73	0.54
1:B:222:LYS:HA	1:B:270:VAL:HG12	1.89	0.54
1:B:203:THR:HG22	1:B:205:LEU:N	2.22	0.54
1:B:30:PHE:C	1:B:51:THR:HG21	2.33	0.54
1:B:218:ARG:HG2	1:B:274:GLU:HG2	1.89	0.53
1:C:144:ILE:HD11	1:C:331:ILE:HD11	1.90	0.53
1:D:170:GLU:HA	1:D:173:LYS:HE3	1.89	0.53
1:D:57:LEU:HD21	1:D:125:ILE:HB	1.91	0.53
1:B:335:TYR:O	1:B:339:ILE:N	2.38	0.52
1:C:63:LEU:HD23	1:C:73:VAL:HG21	1.90	0.52
1:D:253:TYR:CD1	1:D:254:PRO:HA	2.45	0.51
1:B:149:SER:OG	1:B:151:GLU:OE1	2.28	0.51
1:A:303:VAL:HG12	1:A:307:MET:HE2	1.91	0.51
1:C:279:PHE:HD1	1:C:284:GLU:HB2	1.76	0.51
1:D:17:CYS:HB2	1:D:156:TRP:CE3	2.45	0.51
1:C:23:MET:HB2	1:C:126:GLU:OE2	2.10	0.51
1:C:76:LEU:HD23	1:C:128:LEU:HD13	1.92	0.51
1:A:189:PRO:O	1:A:192:GLN:HG2	2.12	0.50
1:B:215:LEU:HD12	1:B:318:ASN:ND2	2.26	0.50
1:B:76:LEU:HD23	1:B:128:LEU:HD13	1.94	0.50
1:C:15:SER:HA	1:C:19:LYS:HD3	1.93	0.49
1:D:103:ILE:HD11	1:D:115:GLU:HB3	1.95	0.49
1:D:73:VAL:HG12	1:D:79:ARG:HH21	1.78	0.49
1:D:65:ARG:NH2	2:D:410:HOH:O	2.45	0.49
1:D:326:ILE:O	1:D:330:LYS:HG2	2.12	0.49
1:B:227:TYR:HB2	1:B:334:LEU:HD12	1.94	0.49
1:D:152:VAL:HG23	1:D:202:PRO:HD3	1.95	0.48
1:D:144:ILE:HD11	1:D:331:ILE:HD11	1.95	0.48
1:A:283:ASP:O	1:A:286:ILE:HG13	2.12	0.48
1:A:199:GLU:OE2	1:A:218:ARG:NH1	2.45	0.48
1:A:323:PHE:O	1:A:327:VAL:HG23	2.14	0.48
1:D:17:CYS:HB2	1:D:156:TRP:HE3	1.78	0.48
1:A:253:TYR:CD1	1:A:254:PRO:HA	2.49	0.48
1:D:50:ASP:OD1	1:D:50:ASP:N	2.44	0.47
1:A:11:LEU:O	1:A:126:GLU:HA	2.13	0.47
1:A:17:CYS:HB2	1:A:156:TRP:CE3	2.49	0.47
1:A:57:LEU:HD22	1:A:86:MET:HE2	1.96	0.47
1:A:44:SER:HB3	1:A:103:ILE:HD13	1.96	0.47
1:A:242:TRP:CZ2	1:A:244:PRO:HB3	2.50	0.47
1:D:125:ILE:HD11	1:D:140:LEU:HD21	1.96	0.47
1:B:145:TYR:CD1	1:B:191:LYS:HG2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:244:PRO:O	2:D:401:HOH:O	2.21	0.47
1:A:188:ASP:OD1	1:A:191:LYS:NZ	2.47	0.47
1:B:17:CYS:SG	1:B:18:GLY:N	2.88	0.46
1:B:197:VAL:HB	1:B:220:ILE:HB	1.96	0.46
1:B:296:SER:O	1:B:332:ARG:NH2	2.48	0.46
1:D:64:ASP:HB2	1:D:109:GLY:O	2.16	0.46
1:B:177:GLU:HG3	1:B:178:ALA:N	2.30	0.46
1:D:151:GLU:H	1:D:151:GLU:CD	2.23	0.46
1:C:326:ILE:O	1:C:330:LYS:HG2	2.16	0.46
1:B:23:MET:HE2	1:B:54:VAL:HG22	1.97	0.46
1:B:326:ILE:O	1:B:330:LYS:HG2	2.16	0.46
1:A:49:SER:HB3	1:A:52:THR:H	1.80	0.45
1:A:298:LYS:HG3	1:A:332:ARG:NH2	2.31	0.45
1:D:298:LYS:HG2	1:D:332:ARG:NH2	2.31	0.45
1:C:64:ASP:O	1:C:68:ARG:HG3	2.17	0.45
1:D:137:ARG:HD3	1:D:193:TYR:CG	2.52	0.45
1:D:154:PHE:O	1:D:158:ILE:HG12	2.16	0.45
1:D:170:GLU:HA	1:D:173:LYS:HG2	1.98	0.45
1:B:279:PHE:N	1:B:317:ASN:O	2.49	0.45
1:A:76:LEU:HD11	1:A:179:ARG:NH2	2.32	0.45
1:A:134:GLU:HG3	1:A:137:ARG:NH1	2.32	0.45
1:C:7:ILE:O	1:C:7:ILE:HG13	2.17	0.44
1:C:312:ASP:OD1	1:C:312:ASP:N	2.39	0.44
1:C:53:THR:HB	1:C:120:PRO:HG3	1.99	0.44
1:B:21:THR:HG23	1:B:313:PHE:CD2	2.52	0.44
1:C:63:LEU:HB3	1:C:68:ARG:HG2	2.00	0.44
1:A:144:ILE:HD11	1:A:331:ILE:CD1	2.40	0.43
1:D:296:SER:HB3	1:D:333:ASP:HB2	2.00	0.43
1:D:189:PRO:O	1:D:192:GLN:HG2	2.19	0.43
1:D:15:SER:HA	1:D:19:LYS:HD3	2.01	0.43
1:C:52:THR:HA	1:C:122:ILE:O	2.19	0.43
1:C:346:ARG:HD3	1:C:346:ARG:HA	1.70	0.43
1:C:292:LEU:HB2	1:C:295:LEU:HD11	2.01	0.43
1:A:62:SER:HB2	1:C:114:PRO:HG2	2.01	0.42
1:D:218:ARG:HG2	1:D:274:GLU:HG3	2.01	0.42
1:B:11:LEU:O	1:B:126:GLU:HA	2.19	0.42
1:B:137:ARG:HD3	1:B:193:TYR:CG	2.55	0.42
1:B:49:SER:OG	1:B:50:ASP:N	2.53	0.42
1:C:176:ILE:O	1:C:179:ARG:HG2	2.19	0.42
1:A:23:MET:HE3	1:A:23:MET:HB3	1.76	0.42
1:A:219:LEU:O	1:A:272:VAL:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:ILE:HD11	1:B:304:THR:HG21	2.02	0.42
1:B:339:ILE:HD13	1:B:339:ILE:HA	1.72	0.42
1:C:65:ARG:NH1	1:C:106:HIS:O	2.52	0.42
1:C:253:TYR:CD1	1:C:254:PRO:HA	2.55	0.42
1:D:38:LYS:HD3	1:D:39:GLY:N	2.34	0.42
1:B:346:ARG:HA	1:B:346:ARG:HD3	1.49	0.42
1:A:346:ARG:NE	1:A:346:ARG:HA	2.35	0.41
1:C:50:ASP:OD1	1:C:50:ASP:N	2.48	0.41
1:A:151:GLU:OE2	1:A:151:GLU:N	2.53	0.41
1:B:327:VAL:O	1:B:331:ILE:HG12	2.20	0.41
1:A:129:HIS:N	1:A:130:PRO:HD3	2.34	0.41
1:C:203:THR:OG1	1:C:276:ASP:OD1	2.36	0.41
1:C:144:ILE:HD11	1:C:331:ILE:CD1	2.50	0.41
1:A:154:PHE:O	1:A:158:ILE:HG12	2.21	0.41
1:A:197:VAL:HB	1:A:220:ILE:HB	2.02	0.41
1:B:203:THR:HG23	1:B:276:ASP:OD1	2.19	0.41
1:C:189:PRO:O	1:C:192:GLN:HG2	2.21	0.41
1:A:137:ARG:HD3	1:A:193:TYR:CG	2.56	0.41
1:B:203:THR:OG1	1:B:214:VAL:O	2.38	0.41
1:A:37:PRO:HG2	1:A:115:GLU:OE1	2.20	0.41
1:B:9:ILE:HD13	1:B:331:ILE:HG21	2.03	0.41
1:C:226:LYS:HE2	1:C:227:TYR:CZ	2.56	0.41
1:A:128:LEU:HA	1:A:128:LEU:HD23	1.89	0.40
1:A:248:LYS:HE3	1:A:287:TYR:OH	2.21	0.40
1:B:312:ASP:OD1	1:B:312:ASP:N	2.39	0.40
1:A:187:ILE:HA	1:A:190:GLN:HE21	1.86	0.40
1:B:217:VAL:HG11	1:B:319:GLY:C	2.46	0.40
1:D:259:ASN:HB2	1:D:274:GLU:HB3	2.02	0.40
1:A:65:ARG:O	1:A:69:LYS:HG3	2.21	0.40
1:B:218:ARG:HG2	1:B:274:GLU:CG	2.52	0.40
1:D:11:LEU:O	1:D:126:GLU:HA	2.22	0.40
1:B:154:PHE:O	1:B:158:ILE:HG12	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries

of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	347/359 (97%)	341 (98%)	6 (2%)	0	100	100
1	B	341/359 (95%)	333 (98%)	8 (2%)	0	100	100
1	C	341/359 (95%)	333 (98%)	8 (2%)	0	100	100
1	D	345/359 (96%)	341 (99%)	4 (1%)	0	100	100
All	All	1374/1436 (96%)	1348 (98%)	26 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	302/312 (97%)	298 (99%)	4 (1%)	61	82
1	B	300/312 (96%)	294 (98%)	6 (2%)	48	75
1	C	300/312 (96%)	289 (96%)	11 (4%)	30	57
1	D	302/312 (97%)	293 (97%)	9 (3%)	36	64
All	All	1204/1248 (96%)	1174 (98%)	30 (2%)	42	69

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	ILE
1	A	272	VAL
1	A	334	LEU
1	A	338	LEU
1	B	49	SER
1	B	177	GLU
1	B	208	ASP
1	B	259	ASN

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Mol	Chain	Res	Type
1	B	312	ASP
1	B	339	ILE
1	C	7	ILE
1	C	29	VAL
1	C	63	LEU
1	C	71	GLN
1	C	158	ILE
1	C	165	ARG
1	C	211	GLU
1	C	222	LYS
1	C	280	ASP
1	C	312	ASP
1	C	344	THR
1	D	7	ILE
1	D	27	THR
1	D	73	VAL
1	D	99	VAL
1	D	217	VAL
1	D	248	LYS
1	D	259	ASN
1	D	282	LEU
1	D	344	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	118	GLN
1	A	305	GLN
1	C	150	ASN
1	C	305	GLN
1	D	45	ASN
1	D	192	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	349/359 (97%)	0.34	20 (5%) 29 26	31, 50, 77, 108	0
1	B	343/359 (95%)	0.31	13 (3%) 44 39	32, 52, 82, 111	0
1	C	343/359 (95%)	0.28	13 (3%) 44 39	33, 51, 78, 113	0
1	D	347/359 (96%)	0.27	8 (2%) 61 57	27, 51, 76, 96	0
All	All	1382/1436 (96%)	0.30	54 (3%) 43 38	27, 51, 78, 113	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	347	ALA	6.0
1	B	343	ALA	5.1
1	C	347	ALA	4.5
1	B	344	THR	3.6
1	A	17	CYS	3.5
1	B	340	ALA	3.5
1	A	20	SER	3.4
1	C	341	ASN	3.3
1	C	343	ALA	3.3
1	A	312	ASP	3.2
1	B	17	CYS	3.2
1	C	17	CYS	3.1
1	B	16	GLY	3.0
1	A	352	LEU	3.0
1	D	17	CYS	3.0
1	C	344	THR	2.8
1	A	347	ALA	2.8
1	A	15	SER	2.7
1	A	349	ALA	2.7
1	B	345	ALA	2.7
1	A	16	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	353	GLU	2.6
1	B	18	GLY	2.6
1	A	300	TYR	2.6
1	D	66	TYR	2.6
1	B	39	GLY	2.5
1	C	162	MET	2.5
1	B	15	SER	2.5
1	A	18	GLY	2.5
1	C	340	ALA	2.5
1	A	351	ALA	2.4
1	D	110	LEU	2.4
1	C	345	ALA	2.4
1	C	342	LYS	2.4
1	A	208	ASP	2.4
1	D	33	ALA	2.4
1	C	14	ASP	2.2
1	C	163	ALA	2.2
1	D	16	GLY	2.2
1	D	109	GLY	2.2
1	C	72	LYS	2.2
1	A	99	VAL	2.1
1	A	7	ILE	2.1
1	A	286	ILE	2.1
1	C	16	GLY	2.1
1	D	338	LEU	2.1
1	B	170	GLU	2.1
1	D	177	GLU	2.1
1	A	168	SER	2.1
1	A	335	TYR	2.1
1	B	174	ALA	2.0
1	A	290	SER	2.0
1	A	34	ALA	2.0
1	B	335	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.